

**IN THE CLAIMS:**

Please amend the claims as follows:

1. (Currently amended) A method of inferring a function of one or more genes, the method comprising:

assembling a distribution of gene expression level measurements **for a given gene over a variety of experimental conditions**, wherein each of **the** gene expression level measurements comprises at least one parameter;

calculating a significance score for each gene expression level measurement in **the** distribution, **wherein the significance scores are outputted to a memory**;

selecting ~~the at least one~~ gene expression level measurements ~~from said distribution based on its~~ **having a predefined** significance score; **and**

comparing ~~the said at least one parameter(s) of the~~ selected at least one gene expression level measurement(s) to ~~the said at least one parameter(s) of the~~ non-selected gene expression level measurements; ~~and to determine the non-overlapping said at least one parameter(s) present in the selected gene expression level measurements but from said selected at least one gene expression level measurement that is not present in the~~ non-selected gene expression level measurements,

**wherein the function of the gene can be inferred based on the non-overlapping parameters.**

2. (Currently amended) The method of claim 1, wherein **the** gene expression level measurements are accessed from a database comprising gene expression level measurements for a plurality of genes.

3. (Currently amended) The method of claim 1, wherein **the** significance score indicates a measure of the distance **the** gene expression level measurements are from a mean value of **the** gene expression level measurements.

4. (Original) The method of claim 3, wherein the significance score is a z-score.

5. (Currently amended) The method of claim 4, wherein the selected ~~said at least one~~ gene expression level measurements have~~[[has]]~~ a z-score greater than 3 and less than -3.

6. (Canceled)

7. (Currently amended) The method of claim 1, wherein the~~[[said]]~~ at least one parameter comprises at least one of ecotype, tissue, RNA type, harvest conditions, genotype, growth conditions, growth media, treatments, and combinations therein.

8. (Currently amended) The method of claim 1, further comprising sorting the expression level measurements based on the~~[[said]]~~ significance scores ~~of said gene expression level measurements~~.

9. (Canceled)

10. (Currently amended) A computer readable medium having instructions for causing a computer to perform a method of inferring a function of one or more genes, the method comprising:

assembling a distribution of gene expression level measurements for a given gene over a variety of experimental conditions, wherein each of the~~[[said]]~~ gene expression level measurements comprises at least one parameter;

calculating a significance score for each gene expression level measurement in the~~[[said]]~~ distribution, wherein the significance scores are outputted to a memory;

selecting ~~the at least one~~ gene expression level measurements from said distribution ~~based on its~~ having a predefined significance score; and

comparing ~~the said at least one~~ parameter(s) of the~~[[said]]~~ selected at least one gene expression level measurement(s) to ~~the said at least one~~ parameter(s) of the non-

selected gene expression level measurements; ~~and to determine~~<sup>[[ing]]</sup> the non-overlapping~~said at least one parameter(s) present in the selected gene expression level measurements but~~<sup>from said selected at least one gene expression level measurement that is not present in</sup> the<sup>[[said]]</sup> non-selected gene expression level measurements,

wherein the function of the gene can be inferred based on the non-overlapping parameters.

11. (Currently amended) The computer readable medium of claim 10, wherein the<sup>[[said]]</sup> gene expression level measurements are accessed from a database comprising gene expression level measurements for a plurality of genes.

12. (Currently amended) The computer readable medium of claim 10, wherein the<sup>[[said]]</sup> significance score indicates a measure of the distance the<sup>[[said]]</sup> gene expression level measurements ~~[[ate-]]~~<sup>are</sup> from a mean value of the<sup>[[said]]</sup> gene expression level measurements.

13. (Original) The computer readable medium of claim 12, wherein the significance score is a z-score.

14. (Currently amended) The computer readable medium of claim 13, wherein the selected ~~said at least one~~ gene expression level measurements have<sup>[[has]]</sup> a z-score greater than 3 and less than -3.

15. (Canceled)

16. (Currently amended) The computer readable medium of claim 10, wherein the<sup>[[said]]</sup> at least one parameter comprises at least one of ecotype, tissue, RNA type, harvest conditions, genotype, growth conditions, growth media, treatments, and combinations therein.

17. (Currently amended) The computer readable medium of claim 10, further comprising sorting the expression level measurements based on the[[said]] significance score of said gene expression level measurements.

18. (Currently amended) A system for inferring a function of one or more genes, the systemmethod comprising:

means for assembling a distribution of gene expression level measurements for a given gene over a variety of experimental conditions, wherein each of the[[said]] gene expression level measurements comprises at least one parameter;

means for calculating a significance score for each gene expression level measurement in the[[said]] distribution, wherein the significance scores are outputted to a memory;

means for selecting theat least one gene expression level measurements from said distribution based on its having a predefined significance score; and

means for comparing thesaid at least one parameter(s) of the[[said]] selected at least one gene expression level measurement(s) to thesaid at least one parameter(s) of the non-selected gene expression level measurements; and to determine[[ing]] the non-overlappingsaid at least one parameter(s) present in the selected gene expression level measurements butfrom said selected at least one gene expression level measurement that is not present in the[[said]] non-selected gene expression level measurements,

wherein the function of the gene can be inferred based on the non-overlapping parameters.

19. (Currently amended) The system of claim 18, wherein the[[said]] gene expression level measurements are accessed from a database comprising gene expression level measurements for a plurality of genes.

20. (Currently amended) The system of claim 18, wherein the[[said]] significance score indicates a measure of the distance the[[said]] gene expression level measurements are from a mean value of the[[said]] gene expression level measurements.

21. (Currently amended) The system of claim 20, wherein the[[said]] significance score is a z-score.

22. (Currently amended) The system of claim 21, wherein the selected ~~said at least one gene expression level measurements~~ have ~~selected has~~ a z-score greater than 3 and less than -3.

23. (Canceled)

24. (Currently amended) The system of claim 18, wherein the[[said]] at least one parameter comprises at least one of ecotype, tissue, RNA type, harvest conditions, genotype, growth conditions, growth media, treatments, and combinations therein.

25. (Currently amended) The system of claim 18, further comprising sorting the expression level measurements based on the[[said]] significance scores ~~of said gene expression level measurements~~.

26. (Canceled)

27. (Currently amended) A computer system useful for inferring functions of genes, the computer system comprising:

a processor;

a memory coupled to the processor;

a display coupled to the processor; and

a computer program that executes on the processor, the program further comprising:

a module assembling a distribution of gene expression level measurements **for a given gene over a variety of experimental conditions**, wherein each of **the** gene expression level measurements comprises at least one parameter,

a module calculating a significance score for each gene expression level measurement in **the** distribution, **wherein the significance scores are outputted to a memory**,

a module selecting ~~the~~ at least one gene expression level measurements ~~from said distribution based on its~~ **having a predefined** significance score,

a module comparing ~~the~~ said at least one parameter(s) of **the** selected at least one gene expression level measurement(s) to ~~the~~ said at least one parameter(s) of **the** non-selected gene expression level measurements, and

a module determining **the non-overlapping** said at least one parameter(s) **present in the selected gene expression level measurements but** ~~from said selected at least one gene expression level measurement that is not present in~~ **the** non-selected gene expression level measurements,

**wherein the function of the gene can be inferred based on the non-overlapping parameters.**

28. (Currently amended) A method of inferring a function of one or more **a** gene(s), the method comprising:

accessing multiple **gene** expression level measurements for multiple samples collected under diversified conditions defined by parameters corresponding to **the** gene;

calculating a score for **each of** the **gene** expression level measurements, **wherein the scores are outputted to a memory**;

selecting **the** samples **having a predefined** ~~based on most significant~~ score;

determining ~~non-overlapped~~ the parameters that are non-overlapped between the selected samples and the samples that were not selected; and

inferring gene function[[s]] from the non-overlapped parameters.

29. (Currently amended) A method for inferring a [[the]] function of a biological molecule, the[[said-]] method comprising:

assembling a distribution of data points from experimental measurements, wherein each of the[[said]] data points comprises at least one parameter;

calculating a significance score for each data point in the[[said]] distribution, wherein the significance scores are outputted to a memory;

selecting ~~at least one of said data~~ the data points based on its having a predefined significance score; and

comparing [[said]] at least one of the parameters [[of]] between the[[said]] selected ~~at least one data point to said at least one parameter of~~ and the non-selected data points; ~~and~~

to determinedetermining the non-overlappingsaid at least one parameter(s) present in the selected data points but~~from said selected at least one data point that is not present in~~ the[[said]] non-selected data points,

wherein the function of the biological molecule can be inferred based on the non-overlapping parameters.

30. (Canceled)